

# Draft Genome Sequence of *Phaeomoniella chlamydospora* Strain RR-HG1, a Grapevine Trunk Disease (Esca)-Related Member of the Ascomycota

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**The Ascomycota species *Phaeomoniella chlamydospora*, in concert with other fungi, is a causal agent for grapevine trunk diseases. Here, we present the first draft of the *P. chlamydospora* genome sequence, which comprises 355 scaffolds, with a total length of 26.59 Mb and 7,279 predicted protein-coding genes.**

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Grapevine trunk diseases, including young esca (Petri disease) and esca proper (black measles), have become some of the most important diseases wherever grapevines are cultivated. The typical symptoms of esca are discolored trunk and white rot, brown spots on fruits, and “tiger stripes” on leaves. Esca is caused or at least supported by the fungal species *Phaeoacremonium aleophilum* (*Togninia minima*), *Phaeomoniella chlamydospora*, and possibly other fungal species (1, 2). A genome draft of strain *P. aleophilum* UCR-PA7 has already been published (3).

The strain *P. chlamydospora* RR-HG1 was isolated from a grapevine trunk (*Vitis vinifera* cv. Rheinriesling) in Illmitz, Austria, in June 2013. The strain was cultivated on malt extract agar and tip purified, and DNA was isolated using the DNeasy plant minikit (Qiagen) for phylogenetic testing by internal transcribed spacer-large subunit (ITS-LSU)/rRNA gene sequencing. The sequencing was performed by GATC Biotech AG (Constance, Germany) using an Illumina MiSeq personal sequencer in paired-end 250-bp mode. A total of 14.51 million reads were received, representing 7,255.1 million bases in total. A read-quality check was performed using FastQC (<http://www.bioinformatics.babraham.ac.uk/>) and PrinSeq (4) and quality filtered using Trimmomatic (5) to obtain 11.74 million paired reads. SPAdes (6) was used for the scaffold assembly. Three hundred fifty-five scaffolds of >10 kb were obtained, with a mean coverage of 170× and a total length of 26.59 Mb. The quality of the genome assembly was assessed in QUAST (7) ( $N_{50}$ , 100,274 bp;  $N_{75}$ , 61,606 bp; length of shortest contig of those covering 50% of the assembly [ $L_{50}$ ], 80 bp;  $L_{75}$ , 166 bp). A sequencing completeness of 96% was calculated using CEGMA (8). Gene annotation was performed using Augustus (9), previously trained on a gene structure created from CEGMA (8), and this method predicted 7,279 genes, the translated sequences of which were submitted to a BLASTp search against the nr database (NCBI).

Since *P. chlamydospora* is a plant pathogen, it can be expected to have a large number of genes putatively coding for plant cell wall-degrading enzymes (10). In our analysis, we predicted 37

beta-glucosidases (cellulose-degrading enzymes), 5 cutinases, 3 pectinases, 10 laccases, one lignin peroxidase, and 49 cytochrome P450 monooxygenases. It was already pointed out by Blanco-Ulate et al. (3) for *P. aleophilum* that these numbers are relatively low compared to those for other wood-degrading fungi.

Another important factor influencing the virulence of phytopathogens is their capacity to produce secondary metabolites (11–14). In RR-HG1, the numbers of genes predicted to be involved in secondary metabolite production, such as those encoding polyketide synthetases (PKS) and nonribosomal peptide synthetases (NRPS), are slightly lower (10 PKS and 12 NRPS genes) than those in other plant pathogens, e.g., *Fusarium graminearum*, with 15 PKS (15) and 15 NRPS (16) genes. This low diversity in secondary metabolite genes might indicate reduced pathogenicity and therefore be a reason why grapevines infected by *P. aleophilum* and *P. chlamydospora* frequently do not show foliar or fruit symptoms (17) or symptoms present only in grapevine plants older than 7 years.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. **JACF00000000**. The version described in this paper is version JACF01000000.

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